

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 20:05:40 ; Search time 571 Seconds
(without alignments)
10211.813 Million cell updates/sec

Title: US-10-089-543-2_COPY_449_1433

Perfect score: 985

Sequence: 1 gatgtaccagtggtggag.....tgagagaatccttcacatc 985

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	985	100.0	1433	6	Abk15699 Cotton fi
2	107.4	10.9	8056	8	Abz10246 Haematopo
3	105.8	10.7	8056	8	Abz10100 Haematopo
C	104.8	10.6	158001	12	Adi17884 Human pho
	104.4	10.6	4985	6	Abq75107 Anopheles
6	104.4	10.6	4985	10	AcF79720 Mosquito
7	102.4	10.4	8222	8	AcF62816 Colon can
8	102.4	10.4	11222	10	AdB54318 Pretreat
C	101.6	10.3	8056	8	Abz10246 Haematopo
	100.8	10.2	8222	8	AcF62794 Colon can
11	100.8	10.2	11222	10	AdB54190 Pretreat
C	100.0	10.2	8056	8	Abz10100 Haematopo
13	96.2	9.8	15548	6	AbL34155 Human imm
14	95.4	9.7	6109	6	AbL32326 Human imm
15	95.4	9.7	6109	6	Aas61077 Human gen
16	94.6	9.6	6963	6	AbL32979 Human imm
17	94.4	9.6	419	8	Abx46069 Bovine ES
C	94.4	9.6	5286	13	AdS89278 Oligonuc
C	94.4	9.6	5286	13	AdS89552 Oligonuc
20	93.6	9.5	9642	6	AbL32357 Human imm

21	91.8	9.3	6216	6	ABK39932	Abk39932 Human che	
22	91.8	9.3	6216	6	ABL70139	ABL70139 Chemical	
23	91.8	9.3	7167	6	ABL32400	ABL32400 Human imm	
24	91.2	9.3	6048	6	ABQ67002	ABQ67002 Human ang	
25	91.2	9.3	12237	6	ABL34358	ABL34358 Human imm	
26	90.8	9.2	7814	4	AAS46530	AAS46530 Tumour su	
27	90.6	9.2	6419	6	ABL32267	ABL32267 Human imm	
28	90.2	9.2	778	6	ABQ15588	ABQ15588 Oligonuc	
C	29	90.2	778	6	ABQ15589	ABQ15589 Oligonuc	
30	90.2	9.2	6175	6	ABL33307	ABL33307 Human imm	
31	90	9.1	18154	6	ABL32254	ABL32254 Human imm	
32	89.6	9.1	6145	6	ABL32972	ABL32972 Human imm	
C	33	89.2	9.1	9789	2	AAI41852	AAI41852 cDNA enco
34	89	9.0	3683	8	ABZ10199	ABZ10199 Haematopo	
C	35	88.6	9.0	6644	2	AAZ33181	AAZ33181 Base sequ
C	36	88.6	9.0	7372	2	AAZ33182	AAZ33182 Base sequ
C	37	88.6	9.0	7797	2	AAZ33180	AAZ33180 Cowpox vi
C	38	88.6	9.0	7996	2	AAZ33184	AAZ33184 Base sequ
C	39	88.4	9.0	3738	3	AAA70178	Plasmodiu
	40	88.4	9.0	5768	6	ABK31192	Signal tr
	41	88.4	9.0	5768	6	ABL70517	Chemical
42	88.4	9.0	5768	6	AAS61105	Human gen	
43	88.4	9.0	6286	4	AAS46591	Tumour su	
44	88.4	9.0	61020	4	AAS46787	Tumour su	
45	88.2	9.0	6292	4	AAS46735	Tumour su	

ALIGNMENTS

RESULT 1
ABK15699
ID ABK15699 standard; DNA; 1433 BP.
XX
AC ABK15699;
XX
DT 21-MAY-2002 (first entry)
XX
DE Cotton fibre-specific beta tubulin, CFTUB2, promoter fragment.
XX
KW Cotton; ds; CFTUB2; fibre-specific beta tubulin; transgenic. promoter;
KW plant; anthocyanin gene; silk protein gene; cotton fibre strength;
KW polyhydroxybutyrate.
XX
OS Gossypium hirsutum.
XX
FH Key Location/Qualifiers
FT Promoter 449..1433
FT /*tag= a
FT /note= "Cotton fibre-specific promoter. This sequence is specifically claimed in claim 3"
XX
PN WO200210377-A1.
XX
PD 07-FEB-2002.
XX
PF 01-AUG-2000; 2000WO-SG000111.
XX
PR 01-AUG-2000; 2000WO-SG000111.
XX
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
PI Cai L, Li X, Cheng N, Liu J;
XX
DR WPI; 2002-217120/27.
XX
PT New fiber-specific beta-tubulin promoter from cotton for controlling gene
PT expression in cotton fibers and creating transgenic plants, in particular
PT cotton plants, having altered fiber characteristics.
XX
PS Claim 2; Fig 2; 3opp; English.
XX
CC The invention relates to a promoter that is cotton fibre-specific,

comprising the promoter of the cotton beta-tubulin gene CFTUB2. The promoter is fibre-specific in cotton and controls specific gene expression at the transcriptional level in cotton fibres and is useful for improving cotton fibres to create new cotton varieties with high fibre quality and yield by gene manipulation. The promoter is useful for creating transgenic plants, in particular cotton having altered fibre characteristics, and permits selective expression of a transgene in the cotton fibre, permitting greater latitude in the types of transgenes employed. Examples of expression of desirable genes in cotton fibre, but not in other parts of the cotton plants, include anthocyanin genes for coloured cotton, silk protein genes from silk worm or spiders for increased strength of cotton fibre, and biosynthesis of polyhydroxybutyrate in cotton fibre for improved thermal properties and insulating characteristics. The promoter can improve cotton fibres to create new cotton varieties with higher fibre quality and yield. The present sequence is the CFTUB2 promoter fragment

Query Match 100.0%; Score 985; DB 6; Length 1433;
Best Local Similarity 100.0%; Pred. No. 4.3e-123;
Matches 985; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGTGACCAAGTGGTGGAGAGAGAGTCTACCGATTGGTCAAGTGGGACCAATTTT 60
DB 449 GATGTGACCAAGTGGTGGAGAGAGAGTCTACCGATTGGTCAAGTGGGACCAATTTT 508
QY 61 TTTTACCTCTCCCTAGATTCCTTAATCTATGCAATTTCTCATTTTCATTTATTT 120
DB 509 TTTTACCTCTCCCTAGATTCCTTAATCTATGCAATTTCTCATTTTCATTTATTT 568
QY 121 AATTATTTTATATTTTGGATAAAATCTAATCTTTTACCTTTTATTTTAAAGAAATTT 180
DB 569 AATTATTTTATATTTTGGATAAAATCTAATCTTTTACCTTTTATTTTAAAGAAATTT 628
QY 181 ATTTAATTTTATATTTTATAGATAAAATCTAATCTTTTACCTTTTATTTTAAAG 240
DB 629 AATTAAATTTTATATTTTATAGATAAAATCTAATCTTTTACCTTTTATTTTAAAG 688
QY 241 AATTCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
DB 689 AATTCAATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 748
QY 301 ATCGGATTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 360
DB 749 ATCGGATTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 808
QY 361 TTAACACATTTTTCGATTAAATTTATATATATATATATATATATATATATATATAT 420
DB 809 TTAACACATTTTTCGATTAAATTTATATATATATATATATATATATATATATATAT 868
QY 421 ATGTTGTCAAT 480
DB 869 ATGTTGTCAAT 928
QY 481 AATTAACTCTTATACCAATTAATTTGAGAGCAATTTATTTTATCTCACCCTC 540
DB 929 AATTAACTCTTATACCAATTAATTTGAGAGCAATTTATTTTATCTCACCCTC 988
QY 541 CATTAATGCAAT 600
DB 989 CATTAATGCAAT 1048
QY 601 TTAACCAATTTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 660
DB 1049 TTAACCAATTTTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1108
QY 661 ATCTGAAAGGCGCAGCTGTCCAGCTGTCCAGCTGTCCAGCTGTCCAGCTGTCCAG 720
DB 1109 ATCTGAAAGGCGCAGCTGTCCAGCTGTCCAGCTGTCCAGCTGTCCAGCTGTCC 1168
QY 721 AACTACATTTGTACGTTACTAAGCAATTCCTCAATTTTCAAAATTCATTTTCCAG 780

Db 1169 AACTACATTTGTACGTTACTAAGCAATTCCTCAATTTTCAAAATTCATTTTCCAGGAA 1228
QY 781 ACGAAACGTCGTTACTAAGCAATTCCTCAATTTTCAAAATTCATTTTCCAGGAA 840
Db 1229 ACGAAACGTCGTTACTAAGCAATTCCTCAATTTTCAAAATTCATTTTCCAGGAA 1288
QY 841 ATCTTTTAACTCTCTAT 900
Db 1289 ATCTTTTAACTCTCTAT 1348
QY 901 ATTTCCGGAATTCCTTTATATATATATATATATATATATATATATATATATATAT 960
Db 1349 ATTTCCGGAATTCCTTTATATATATATATATATATATATATATATATATATATAT 1408
QY 961 GAAATATGAGAGAAATCCTTCATC 985
Db 1409 GAAATATGAGAGAAATCCTTCATC 1433

RESULT 2
ABZ10246
ID ABZ10246 standard; DNA; 8056 BP.
XX
AC ABZ10246;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
OS Homo sapiens.
XX
PN WO200277272-A2.
XX
PD 03-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorian P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwöpe I, Ziebarth H;
XX
DR WPI; 2003-018942/01.
XX
PT Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
PS
XX
XX Claim 28; SEQ ID NO 386; 117pp; English.
CC The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the

CC	amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
XX	
SQ	Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
	Query Match 10.9%; Score 107.4; DB 8; Length 8056;
	Best Local Similarity 51.1%; Pred No. 4.8e-06;
	Matches 305; Conservative 0; Mismatches 286; Indels 6; Gaps 2
Qy	52 AAATTTTATTATTCACCTCGCCTAGATTCGTAATACTATTGCATTATTCATCTCATTTTCAT 111
Db	55 AAAATTTTTTTTAAATTTTTTTTTTAAATTTTTTAAATTTTTTATATTTTTTATATATAAT 114
Qy	112 TATTTATTTAATTAATTTATATTAATTTTGGAATAAAATTCCTAATACTTTTACTTTTTTAA 171
Db	115 TATTATTTTAAATTTTTTATATTTTTTTTATTTATTTATTTTTTATTTTTTATTTATTTT -- 172
Qy	172 AAGCAATTTATTTAAATTTATTTATATTTATAGATAAAAAATTCATAACTTTTACTTTTTT 231
Db	173 TATTATTTTTTTTAAATTAATTAATTTTAAATTAATTAATTTTAAAANAATTTTTAAA 232
Qy	232 TTTAAAAAGAATTTCAAFTGGTGTTTTTTCTTAAATTTAGTTTTTAACTTATCTATAATTA 291
Db	233 ATTTTAAAAAATTTAAAAATTTTAAAAATTTTAAATTTTAAATTTTAAAAAANAATTTT 292
Qy	292 AAAATTCGATCGGATTAGTGTGTCGAAAGTCAAGTCACATGAATTTTGTGGAGAAA 351
Db	293 ATTFTTTTTTAAAAATTAATTTTTTAAAAAANAATTAATTAATAAATAAATAAATAATA 352
Qy	352 AAATABAAAATTAACACACATTTTTTCGATTAATTTTATATATATATAATTAATTAACACAT 411
Db	353 ATTTAAAAAANAANAANAATGAATAATTTTAAATTTTAAAAATTTTAAATTTTAAATAAT 412
Qy	412 TTTTATTTAATGT----TGTCAAATAAATTTTTTAAATTTTAAATTTTTCAGCACACAATTAC 467
Db	413 ATTTATTAATTTATTTTATTTTTTTTTTAAAAATAATAAAAAANAATTAATTTTAAAAATA 472
Qy	468 ACTCTCATCATAAATTTAACTTTATTACCATAAATTAATAATTTGTGAGGACAAATTTT 527
Db	473 AATATATTTAAATTAATAAANAATTTAAATTTTATATTTTAAATTAATTAATTAATATAT 532
Qy	528 TAATCTCACCCCTCAATTAATGCATATTTATTAATTTTGTTCGATCTCTTATTTTCATC 587
Db	533 TAAAAATTTAAATTTTATATAAATTTATAPAAAATGTTTTTATTTAAAAATTTATTTATTTA 592
Qy	588 CTACATTTAATCATTTAACCCAATTTTGAACGTGTTATATAATTTCTTAACTTTATTCAC 644
Db	593 ATAATATTTTAAAAAANAATTTATATAAATTTTAAAAATTTTAAAAAATAATTTTAA 649
RESULT 3	
ABZ10100	
ID	ABZ10100 standard; DNA; 8056 BP.
XX	
AC	ABZ10100;
XX	
DT	16-JAN-2003 (first entry)
DE	Haematopoietic cell proliferation disorder related DNA sequence #240.
XX	
KW	Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
OS	Homo sapiens.
XX	
PX	WO200277272-A2.
XX	

PD	03-OCT-2002.
XX	
PF	26-MAR-2002; 2002WO-EP003401.
XX	
PR	26-MAR-2001; 2001US-0278333P.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI	Olek A, Pispembrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI	Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI	Schwöpe I, Ziebarth H;
XX	
DR	WFI; 2003-018942/01.
XX	
PT	Detecting and differentiating between hematopoietic cell proliferative
PT	disorders, comprises contacting a target nucleic acid with a reagent that
PT	distinguishes between methylated and non-methylated CpG dinucleotides.
XX	
PS	Claim 28; SEQ ID NO 240; 117pp; English.
XX	
CC	The present invention describes a method for detecting and
CC	differentiating between haematopoietic cell proliferative disorders
CC	associated with at least 1 gene and/or their regulatory regions in a
CC	subject. The method comprises contacting a target nucleic acid in a
CC	biological sample obtained from the subject with at least 1 reagent,
CC	which distinguishes between methylated and non-methylated CpG
CC	dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
CC	represent specifically claimed nucleotide sequences from the present
CC	invention. Oligonucleotides from the present invention can be used: for
CC	differentiating between healthy haematopoietic cells and proliferative
CC	disorder haematopoietic cells; for differentiating between acute
CC	lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC	determining the cytosine methylation state and/or single nucleotide
CC	polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC	related sequences and their complements; and as primers for the
CC	amplification of haematopoietic cell proliferation disorder related DNA
CC	sequences. The nucleotide sequences from the present invention can also
CC	be used for detecting a predisposition to, differentiation between
CC	subclassses, diagnosis, prognosis, treatment and/or monitoring of
CC	haematopoietic cell proliferative disorders. The present method enables a
CC	highly specific classification of haematopoietic cell proliferative
CC	disorders allowing for improved and informed treatment of patients
XX	
SQ	Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;
	Query Match 10.78; Score 105.8; DB 8; Length 8056;
	Best Local Similarity 50.94; Pred. No. 7.9e-06;
	Matches 304; Conservative 0; Mismatches 287; Indels 6; Gaps 2
QY	52 AATTTTATTATTTACCTCGCCTAGATTTCGTAATACTACTTGCACTTTATCTCATTTTCAT 111
DB	55 AAATTTTTTTTTTATTTTTTTTTTTTTTAAATTTTAAATTTTATTTTTTATATTTAAT 114
QY	112 TATTATTTTAAATTTATTTATTTATTTATTTGGATAAAAAATCTTAATACTTTACTTTTTTAA 171
DB	115 TAATTATTTTAAATTTTTTATTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTT - 172
QY	172 AAGAATTTATTTAATTTATTTTATTTATTTTAGATAAAAATCTCAATACTTTACTTTTTT 231
DB	173 TATTATTTTTTTTAAATTTATTTAATTTTAAATTTTATTTAATTTTAAAAAATATTTTAA 232
QY	232 TTTTAAAAAGAAATTTCAATTGCGTTTTTTCCTAAATTTAGTTTAAATCTTATACTAATATA 291
DB	233 ATTTTAAAAAATTTAAAAAATTTTAAAAATTTTAAATTTTATTTTAAATAAAAAATTTT 292
QY	292 AAAAATCTGATCGAATTAGTGGTGTGCAAAGTCACATGAATTTTGTGTGGAGAAA 351
DB	293 ATTITTTTTTAAATTTATTTTTTTTAAAAAATAATTTAATAAAAAATAAATAATAATA 352
QY	352 AATAAAAAATTAACAACATTTTTTCGATTAATTTTATTTATATATATAATAATAAACACAT 411
DB	353 ATTTAAAAAATAAAAAACGAAATATAAATATTTTATAATTTTAAAAATTTAAATTTAATAAT 412

[illegible]

[illegible]

QY 587 CCTAACATTATCAATTAACCCAAATTTGACGTGTTAATATTTCTTAACCTATTACTACTATT 646
Db 7852 TTTTATT 7911

QY 647 GT 648
Db 7912 TT 7913

RESULT 9
ABZ10246/c
ID ABZ10246 standard; DNA; 8056 BP.
XX
AC ABZ10246;
XX
DT 16-JAN-2003 (first entry)
XX
DE Haematopoietic cell proliferation disorder related DNA sequence #386.
XX
KW Human; haematopoietic cell proliferation disorder; cytostatic;
KW gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX
OS Homo sapiens.
XX
XX WO200277272-A2.
XX
PD 03-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-EP003401.
XX
PR 26-MAR-2001; 2001US-0278333P.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
PI Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, Pelet C;
PI Schwöpe I, Ziebarth H;
XX WPI; 2003-018942/01.
XX
XX Detecting and differentiating between hematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX
PS Claim 28; SEQ ID NO 386; 117pp; English.
XX
XX The present invention describes a method for detecting and
CC differentiating between haematopoietic cell proliferative disorders
CC associated with at least 1 gene and/or their regulatory regions in a
CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients
XX
XX Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

Query Match 10.3%; Score 101.6; DB 8; Length 8056;
Best Local Similarity 49.4%; Pred. No. 2.9e-05;
Matches 291; Conservative 0; Mismatches 296; Indels 2; Gaps 1;
QY 53 ATTTTATTATTTTACCTCTGCTAGATTTCGTAATACATATTCGATTATCTCATTTTCATT 112
Db 2420 ATTTTATTATTTTCAAAAAATAATAAAATTTTAATAATTTATATAAAAAATAAAA 2361
QY 113 ATTTTATTATTTTATATATTTATTTTGGATAAAAATCTATATCTTTTACTTTTTTAAAA 172
Db 2360 ATTATATTAAAAATTAATAAAATTTATTTAAATACAAAAATTAATAAAATTTTAAAA 2301
QY 173 AAGAAATTTATTAATTTTATATATTTATAGATAAAAAATCTATATCTTTTACTTTTTT 232
Db 2300 AATAAATAAATTAATAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 2241
QY 233 TTAAGAGAAATTTCAATTCGCTTTTCTTAAATTTAGTTTAAATCTATATCTATATAA 292
Db 2240 TTTATTAATAATTAATAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 2181
QY 293 AAATTTCTGATCGATTAGTGTGTCAAAGTCACATGAATTTTGTGGAGAAAA 352
Db 2180 TAAATTT--ATAATTTTATTTTATTTTATTTTATTTTAAATAAAAAATTAATA 2123
QY 353 AATAAAAAATTAACACATTTTTCGATTAATTTATATATATATATATATATATAACACATT 412
Db 2122 AAATTTATTAATAAATTTTATTAATTTTATTAATTTTAAATTTTAAATTTTAAAT 2063
QY 413 TTTATTTAATGTTGTCATAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 472
Db 2062 TTTTAAATAAATAAATAATTTTAAATAATATTTTATTTTAAATAATATTTTAAATTTTAT 2003
QY 473 CATCAATTAATTTAATCTTTATTTACCAATAATTTAAATTTTAAATTTTAAATTTTAAAT 532
Db 2002 TAAATTTTAAATAAATAAATAATTTTAAATAATTTTATTTTAAATAAATAATTTTATTT 1943
QY 533 TCACCTCTCAATTAATGCTATATTTAAATTTTGTTCGATATCTTTTATTTCTACTCTTAAC 592
Db 1942 TATATTTAATAATTTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 1883
QY 593 ATTAATCATTAACCAATTTTGAACGTGTATAATTTCTTAACCTTATTTCA 641
Db 1882 AAAAAATAATTAATAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 1834

RESULT 10
ACF62794
ID ACF62794 standard; DNA; 8222 BP.
XX
XX ACF62794;
AC ACF62794;
XX
DT 09-OCT-2003 (first entry)
XX
DE Colon cancer analysis related genomic DNA SEQ ID NO:43.
XX
KW Human; colon cancer; oestrogen receptor; myoglobin; p21; p27; p16; p53;
KW progesterone receptor; pcna; cea; cdcs; c-erbB2; methylation; CpG;
KW characterization; classification; diagnosis; differentiation;
KW colon cell proliferative disorder; gene; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO2003014388-A2.
PN
PD 20-FEB-2003.
XX
XX 09-AUG-2002; 2002WO-EP008939.
PF
XX 09-AUG-2001; 2001DE-01039283.
PR
XX (EPIG-) EPIGENOMICS AG.
PA
XX

[illegible]

[illegible]

Qy	533	TCACCCTCCATTAATGCAATTAATAATTTTGGTTCGATACACTCTTATTTCACCTCTAAC	592
Db	2105	TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT	2164
Qy	593	ATTAATCATTAACCCAAATTTGAACTGGTTATATAATTTCTTAACTTATTCACATTTG	647
Db	2165	ATTTATTTATTTATTTATTTATTTAAATTTATTTATTTATTTATTTATTTATTTATTTAGTGT	2219

Search completed: March 14, 2005, 23:50:30
Job time : 575 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	985	100.0	1433	6	AX370650	Sequence
2	981.8	99.7	5765	8	AF487511	Gossypium
3	119.2	12.1	170827	2	AC125567	Rattus no
C 4	113.2	11.5	68626	3	PFWAL3P5	AL034556 Plasmodiu
C 5	112.8	11.5	67970	3	PFWAL3P5	AL0311746 Plasmodiu
C 6	111.2	11.4	180861	2	CR391970	Danio rer
7	112.2	11.3	286208	2	AC117140	Rattus no
C 8	110.2	11.2	258658	3	AE014832	Plasmodiu
C 9	110	11.2	191191	2	CR847965	Danio rer
C 10	109.8	11.1	348174	3	CR382399	Plasmodiu
C 11	109.6	11.1	169056	2	CR536620	Danio rer
C 12	109.6	11.1	213093	5	BX347875	Zebrafish
13	109.2	11.1	110000	2	PFWAL8P1_12	Continuation (13 o
C 14	109.2	11.1	197951	2	CR392343	Danio rer
C 15	109.2	11.1	246611	2	AC111404	Rattus no
C 16	108.4	11.0	145925	5	BX842571	Zebrafish
C 17	108.4	11.0	150000	2	BX927162_2	Continuation (3 of
C 18	108.4	11.0	192182	5	BX649602	Zebrafish
C 19	108.2	11.0	140289	5	BX005458	Zebrafish

Db 569

QY 181 ATTTAATTATTTTATATATTAGATAAAAATCTAATACTTTTCTTTTAAAG 240

Db 893 AATTAACTTATTACCAATAATAAATGTGAGGACAATTAATTTTAACTCACCCTC 952

Qy 541 CATTAAATGATATTAATTAATTTTGTGATACACTTCTTATTTTCACTCCTAAACATTAATCA 600

Db 953 CATTAAATGATATTAATTAATTTTGTGATACACTTCTTATTTTCACTCCTAAACATTAATCA 1012

Qy 601 TTAACCCAAATTTGAACCTGTTAATTTTCTTAACCTTATTTTCACTATTTGGCTCTGGTCC 660

Db 1013 TTAACCCAAATTTGAACCTGTTAATTTTCTTAACCTTATTTTCACTATTTGGCTCTGGTCC 1072

Qy 661 ATCTGAAAGGCCACCGTCCAGCTGTCCAAACACACACTTTTGCACGTCATCAATTTCCAGT 720

Db 1073 ATCTGAAAGGCCACCGTCCAGCTGTCCAAACACACTTTTGCACGTCATCAATTTCCAGT 1132

Qy 721 AACTACATTTGTACAGTTACTTAAGCAAAATCCCAATTTTCAAAAATTTCAATTTTCCAGGAAA 780

Db 1133 AACTACATTTGTACAGTTACTTAAGCAAAATCCCAATTTTCAAAAATTTCAATTTTCCAGGAAA 1192

Qy 781 ACGAAACGTCGTTACTTAACGACCTAAACCCAGCTCAACCTGCGGTCAATTAACGGAA 840

Db 1193 ACGAAACGTCGTTACTTAACGACCTAAACCCAGCTCAACCTGCGGTCAATTAACGGAA 1252

Qy 841 ATCTTTTAACTCTCTATATAACCAAAACCACTCTCATCACCATTTTCCCAATAAAAGA 900

Db 1253 ATCTTTTAACTCTCTATATAACCAAAACCACTCTCATCACCATTTTCCCAATAAAAGA 1312

Qy 901 ATTTCGGGAATTTCTTATTTCTTTTATTTTCTTCTTCCAAATTTCCGTCATTTTCCCGA 960

Db 1313 ATTTCGGGAATTTCTTATTTCTTTTATTTTCTTCTTCCAAATTTTCCGTCATTTTCCCGA 1372

Qy 961 GAAATGAGAGAAATCTTTCATC 985

Db 1373 GAAATGAGAGAAATCTTTCATC 1397

RESULT 3

AC125567

LOCUS

DEFINITION Rattus norvegicus clone CH230-9H22, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.

ACCESSION AC125567

VERSION AC125567.5 GI:24817949

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 170627)

AUTHORS Muzny, D. Marie., Metzker, M. Lee., Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,

Lorensuhera, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mayhoney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Sneed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villanana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlecyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.

Direct Submission

2 (bases 1 to 170627)

Worley, K. C.

Direct Submission

Submitted (29-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 170627)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 9, 2002 this sequence version replaced gi:23096537.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with 'Ns' to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Genome Center

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GDDV

Center clone name: CH230-9H22

Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 162619 bases at least Q40

Consensus quality: 164392 bases at least Q30

Consensus quality: 165269 bases at least Q20

Estimated insert size: 165231; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 109158: contig of 109158 bp in length
* 109159 109258: gap of unknown length
* 109259 109280: contig of 1022 bp in length
* 110281 110380: gap of unknown length
* 110381 111540: contig of 1160 bp in length
* 111541 111640: gap of unknown length
* 111641 170627: contig of 58987 bp in length.

FEATURES

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/db_xref="taxon:10116"
/clone="CH230-9H22"

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misc_feature 3636..4924
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site:EcoRI
end_sequence:BH341988"

ORIGIN

Query Match 12.1%; Score 119.2; DB 2; Length 170627;
Best Local Similarity 50.2%; Pred. No. 6.4e-07;
Matches 295; Conservative 0; Mismatches 293; Indels 0; Gaps 0;

QY 58 TTATTTTACTCTGCTAGATCGTAATACTATGCTATTCATTTTCATTTTATTTA 117
DB 28563 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 28622
QY 118 TTTAATTTTATTTATTTATTTGATATAAAATCTAATCTTTACTTTTTTAAAGAA 177
DB 28623 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 28682
QY 178 TTTAATTTTATTTATTTATTTAGATAAAATCTAATCTTTACTTTTTTAA 237
DB 28683 TTTAATTTTAAATATTTATTTTATTTTATTTTATTTTATTTTATTTAT 28742
QY 238 AAGAAATTTCAATTCGCTTTTCTTAATTTAGTTTAAATCTATCTAATATAAAAT 297
DB 28743 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 28802
QY 298 CTGATCGATTAGTGTGCTCAAGTCAAGTCACATGAATTTGTGAGAGAAATAA 357
DB 28803 TTTATAAATAATTAATTTTATTTTATTTTATTTTAAATAATATTTTAAAT 28862
QY 358 AATTAACACATTTTTCGATTAATTTATTTATTTATTTATTTATTTATTTAT 417
DB 28863 TTTATTATTAATAAATATTTTATTTTATTTTATTTTATTTTATTTATTT 28922
QY 418 TTAATGTGTCAATAATATTTTAAATTTAAATTTTCAAGCACAATTTACACT 477
DB 28923 TTTTATTTATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTAT 28982
QY 478 TTAATTTTATCTTTATTAACATAATTTAAATTTGTGAGGACAAATTTTAA 537
DB 28983 TATTAATTTATTTTATTTATTTATTTATTTTATTTTATTTTATTTTAT 29042
QY 538 CTCATTAATGCAATATTTATTTTATTTTGTGCTGATCTCTTATTTTACCT 597
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QY 598 TCATTAAACCAATTTTGAACCTGTTAATAATTTCTTAACCTTTATTCACAT 645
DB 29103 TTTTTCATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 29150

RESULT 4

PFMAL3P5/c
LOCUS
DEFINITION
ACCESSION

PFMAL3P5
Plasmodium falciparum MAL3P5, complete sequence.
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162

VERSION
KEYWORDS

AL034556.4 GI:23477013
HTG; centromere; CTRP protein; initiation factor E4;
Serine/threonine protein phosphatase.

SOURCE
ORGANISM

Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7

REFERENCE
AUTHORS

1 (bases 1 to 86826)
Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T.,
Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,
Gentles, S., Gilliam, R., Hamlin, N., Harris, D., Holroyd, S.,
Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J.,
Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A.,
Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S.,
Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and
Barrell, B.G.

TITLE
JOURNAL

The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum
Nature 400 (6744), 532-538 (1999)

MEDLINE
PUBMED

99376085
10448855

REFERENCE
AUTHORS

2
Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D.,
Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K.,
Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C.,
Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Corton, C.,
Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J.,
Feltwell, T., Goble, A., Goodhead, I., Gilliam, R., Hamlin, N.,
Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S.,
Horrocks, P., Humphray, S., Jagels, K., James, K.D., Johnson, D.,
Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N.,
Lawson, D., Lennard, N., Line, A., Maddison, M., McLean, J., Mooney, P.,
Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A.,
Rabbinowitzsch, E., Rajandream, M.A., Rutter, S., Rutherford, K.M.,
Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R.,
Squares, S., Stevens, K., Taylor, K., Tivey, A., Unwin, L.,
Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and
Barrell, B.G.

TITLE
JOURNAL

Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13
Nature 419 (6906), 527-531 (2002)

MEDLINE
PUBMED

22255708
12368867

REFERENCE
AUTHORS

3 (bases 1 to 86826)
Lawson, D., Bowman, S. and Barrell, B.

Direct Submission
Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
UK

CB10 15A,
On Oct 2, 2002 this sequence version replaced gi:7711064.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P_falciparum.

Location/Qualifiers
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new exon 2, revised: incorporated new intron in last exon
in comparison with P. knowlesi and P. yoelii"
/codon_start=1

COMMENT

FEATURES

source

gene

CDS

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hume, J., Hulyk, S., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lornshuwa, L., Loulseg, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Maindardine, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nwaokeme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valdes, R., Vera, V., Villaseca, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G., and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 286208)
Worley, K. C.

Direct Submission
Submitted (08-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 286208)
Rat Genome Sequencing Consortium.

Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 6, 2002 this sequence version replaced gi:23097379.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GUCU
Center clone name: CH230-365F7
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 125022 bases at least Q40
Consensus quality: 128107 bases at least Q30
Consensus quality: 129968 bases at least Q20
Estimated insert size: 130783; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 47440: contig of 47440 bp in length
* 47441 47540: gap of unknown length
* 47541 230268: contig of 182728 bp in length
* 230269 230368: gap of unknown length
* 230369 254735: contig of 24367 bp in length
* 254736 254835: gap of unknown length
* 254836 275940: contig of 21105 bp in length
* 275941 276040: gap of unknown length
* 276041 277252: contig of 1212 bp in length
* 277253 277353: gap of unknown length
* 277353 278593: contig of 1141 bp in length
* 278594 282220: contig of 3627 bp in length
* 282221 284049: gap of unknown length
* 284050 284149: gap of unknown length
* 284150 286208: contig of 2059 bp in length.
Location/Qualifiers
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/mol_type="genomic DNA"
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230369..232081
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clone_end:Sp6"
misc_feature
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Best Local Similarity 50.3%; Pred. No. 6.1e-06;
Matches 300; Conservative 0; Mismatches 293; Indels 3; Gaps 1;
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Db 229419 AATTTTCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 229478
QY 113 ATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 172

Db	229479	TATTTTTTTATTTCTTTTTTTTTTTTATTTATATAAAAAATTTTCTAAATTTTATTTTTTTATTTTATTTT	229533
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QY	293	AAATCTCATCGGATTTAGTGTGTTCAAGTCACATGAATTTTGTGTGGAGAAA	352
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QY	533	TCACCTCATTAATGATATTTATTTAAATTTTGTTCGATCTCTTATTTTCACTCCTAAC	592
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RESULT 8			
AE014832/c			
LOCUS	AE014832	258658 bp	DNA linear INV 07-OCT-2002
DEFINITION	Plasmodium falciparum 3D7 chromosome 10 section 4 of 7 of the complete sequence.		
ACCESSION	AE014832		
VERSION	AE014832.1		
KEYWORDS	GI:23495046		
SOURCE	Plasmodium falciparum 3D7		
ORGANISM	Plasmodium falciparum 3D7		
REFERENCE	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
AUTHORS	1 (bases 1 to 258658) Gardner,M.J., Hall,N., Fung,E., White,O., Berriman,M., Hyman,R.W., Carlton,J.M., Pain,A., Nelson,K.E., Bowman,S., Paulsen,I.T., James,K., Eisen,J.A., Rutherford,K., Salzberg,S.L., Craig,A., Kyes,S., Chan,M.-S., Nene,V., Shallow,S.J., Suh,B., Peterson,J., Angiuoli,S., Pertea,M., Allen,J., Selengut,J., Haft,D., Mather,M.W., Vaidya,A.B., Martin,D.M.A., Fairlamb,A.H., Fraunholz,M.J., Roos,D.S., Ralph,S.A., McFadden,G.I., Cummings,L.M., Subramanian,G.M., Mungall,C., Venter,J.C., Carucci,D.J., Hoffman,S.L., Newbold,C., Davis,R.W., Fraser,C.M. and Barrell,B.		
TITLE	Genome sequence of the human malaria parasite Plasmodium falciparum		
JOURNAL	Nature 419 (6906), 498-511 (2002)		
PUBMED	12368864		
REFERENCE	2 (bases 1 to 258658)		
AUTHORS	Gardner,M.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (13-SEP-2002) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA		
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gene			

ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 191191)
McLay, K.
Direct Submission
Submitted (10-OCT-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 11, 2004 this sequence version replaced gi:54019775.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
Center project name: zC232P21
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 187123 bases at least Q40
Consensus quality: 187569 bases at least Q30
Consensus quality: 188211 bases at least Q20
Insert size: 190391; sum-of-contigs
Insert size: 198701; 0.8% error; agarose-fp
Quality coverage: 8.46x in Q20 bases; sum-of-contigs Quality
coverage: 8.18x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2245: contig of 2245 bp in length
* 2246 2345: gap of 100 bp
* 2346 10805: contig of 8460 bp in length
* 10806 10905: gap of 100 bp
* 10906 19399: contig of 8494 bp in length
* 19400 40466: contig of 20967 bp in length
* 40467 40566: gap of 100 bp
* 40567 72373: contig of 31807 bp in length
* 72374 72473: gap of 100 bp
* 72474 132240: contig of 59767 bp in length
* 132241 132340: gap of 100 bp
* 132341 148848: contig of 16508 bp in length
* 148849 148948: gap of 100 bp
* 148949 163725: contig of 14776 bp in length
* 163726 163825: gap of 100 bp
* 163826 191191: contig of 27367 bp in length.

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/db_xref="taxon:7955"
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148949..163724
/note="assembly_fragment:00229"
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ORIGIN

Query Match 11.2%; Score 110; DB 2; Length 191191;
Best Local Similarity 50.0%; Pred. No. 9.5e-06;
Matches 302; Conservative 0; Mismatches 300; Indels 2; Gaps 1;
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DB 10538 TTATTTATTTATTTTAAATAAATATTTATTTATTTATTTATTTATTTATTT 10479
QY 114 TTTATTTAAATTTATTTATTTATTTGGATATAAAATTCATACTTTTAAAA 173
DB 10478 ATTATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 10419
QY 174 AGAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 233
DB 10418 TTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 10359
QY 234 TAAAGAAATTTCAATTCGGTGGTCTTCTTA--ATTAGTTTAAATTCCTATTAATA 291
DB 10358 TATATAAATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 10299
QY 292 AAAATTCGTATCGGATTTAGTGTGTCAAAAGTCAAGTCAATGAATTTTGTGGAGAAA 351
DB 10298 AAAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 10239
QY 352 AAATAAATTTAAACACATTTTCGATTAATTTATTTATTTATTTATTTATTTATTTATTT 411
DB 10238 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 10179
QY 412 TTTTATTTAAATTCGTCAATAATATTTTAAATTTAAATTTTAAATTTTAAATTTTAAATTT 471
DB 10178 TAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 10119
QY 472 TCATCATTTAAATTTAAATCTTATTTACCATTAATTTAAATTTGTGGAGCAATTTTAAAT 531
DB 10118 TATTAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 10059
QY 532 CTCACCTCCATTAATGATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 591
DB 10058 ATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 9999
QY 592 CATTATCATTTAAACCAATTTTGAACACTGTTATTAATTTCTTAACCTTATTCACATTTGTGGC 651
DB 9998 ATATATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAC 9939
QY 652 TCTG 655
DB 9938 TCAG 9935

RESULT 10
CR382399/c
LOCUS
DEFINITION
Plasmodium falciparum chromosome 6, complete sequence; segment 2/5.
ACCESSION
CR382399.1
VERSION
CR382399.1 GI:46361038

[illegible]

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 23:13:46 ; Search time 209 Seconds
(without alignments)
7711.639 Million cell updates/sec

Title: US-10-089-543-2_COPY_449_1433

Perfect score: 985

Sequence: 1 gatgtaccagtggtgag.....tgagagaatccttcacatc 985

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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- 4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	101.8	10.3	612	4	US-09-902-540-1357
C 2	90.2	9.2	5919	4	US-09-949-016-13504
C 3	88.8	9.0	55866	4	US-09-949-016-15129
C 4	88.2	9.0	205044	4	US-09-949-016-15851
C 5	88.2	9.0	205044	4	US-09-949-016-15852
C 6	88.2	9.0	205044	4	US-09-949-016-15853
C 7	88.2	9.0	223471	4	US-09-949-016-12387
C 8	88.2	9.0	223471	4	US-09-949-016-12724
C 9	88.2	9.0	223471	4	US-09-949-016-12725
C 10	87.4	8.9	61178	4	US-09-949-016-17369
C 11	87	8.8	19124	2	US-08-487-826B-13
C 12	85.8	8.7	187169	4	US-09-949-016-12776
C 13	85.8	8.7	191569	4	US-09-949-016-15940
C 14	84.4	8.6	1039	4	US-09-902-540-12880
C 15	84.2	8.5	263693	4	US-09-949-016-12386
C 16	84.2	8.5	263694	4	US-09-949-016-16915
C 17	84	8.5	20674	3	US-09-641-638-651
C 18	84	8.5	20674	4	US-10-170-097-651
C 19	83.8	8.5	147382	4	US-09-949-016-14624
C 20	83.6	8.5	601	4	US-09-949-016-30530
C 21	83.6	8.5	601	4	US-09-949-016-30531
C 22	83.6	8.5	601	4	US-09-949-016-37149
C 23	83.6	8.5	601	4	US-09-949-016-37150
C 24	83.6	8.5	601	4	US-09-949-016-37163
C 25	83.6	8.5	601	4	US-09-949-016-37164
C 26	83.6	8.5	601	4	US-09-949-016-145867
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30	83.6	8.5	601	4	US-09-949-016-146403	Sequence 146403,
31	83.6	8.5	601	4	US-09-949-016-146404	Sequence 146404,
32	83.4	8.5	615	3	US-08-998-416-186	Sequence 186, App
33	83.4	8.5	837	3	US-08-998-416-288	Sequence 288, App
C 34	82.6	8.4	19438	4	US-09-949-016-12899	Sequence 12899, A
C 35	81.6	8.3	18773	4	US-09-949-016-14164	Sequence 14164, A
C 36	81.6	8.3	95255	4	US-09-949-016-17067	Sequence 17067, A
37	81	8.2	18773	4	US-09-949-016-14164	Sequence 14164, A
38	80.8	8.2	636	3	US-08-998-416-1137	Sequence 1137, Ap
39	80.6	8.2	658	3	US-08-998-416-595	Sequence 595, App
40	80.2	8.1	29717	4	US-09-949-016-16284	Sequence 16284, A
41	80.2	8.1	60376	4	US-09-949-016-12423	Sequence 12423, A
42	79.8	8.1	134987	4	US-09-949-016-15348	Sequence 15348, A
43	79.8	8.1	134987	4	US-09-949-016-15349	Sequence 15349, A
44	79.8	8.1	134987	4	US-09-949-016-15350	Sequence 15350, A
45	79.8	8.1	134987	4	US-09-949-016-15507	Sequence 15507, A

ALIGNMENTS

RESULT 1

US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447

GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2003-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 1357

; LENGTH: 612

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(612)

; OTHER INFORMATION: unsure at all n locations

US-09-902-540-1357

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Best Local Similarity 48.1%; Pred. No. 2.6e-10;
Matches 286; Conservative 0; Mismatches 309; Indels 0; Gaps 0;

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Qy	174	AGAAATTTATTTAATTTATTTATTTATTTAGATAAAATTTCTAATACTTTTACTTTTT	233
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Qy	234	TAAAAGAAATTTCAATTTGGTTTTTTTCTTAATTTAGTTTATTTCTTACTATAATAA	293
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Qy	294	AATTCGTGCGGATAGTGTGGTGTCAAAGTCAAAGTCACATGAATTTTGTGGAGAAAA	353
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QY 390 ATATATAATAATAAACACATTTTATTTTAAATGTTGTCATTAATAATATTTTAAATAAAA 449
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QY 450 TTTCAGCACAACAATTACACTCTCATCAT-TAAATTTAATCTTATTTACCATTAATTAATAAT 508
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QY 509 TGTGAGGACAAATTTTATTTTATCTCACCTCCATTAATGCAATATTTAATTTTGTTC 568
Db 4873 ATACAGCCATTTTCTTAAATAAATAACAGCCATTTTCTTAAATATATATTTTTCCTTT 4814
QY 569 GATACTTCTTATTTCACTCTCTA 590
Db 4813 TAAACITTTTTCCTTTTCCCA 4792

RESULT 4
US-09-949-016-15851/c
; Sequence 15851, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15851
; LENGTH: 205044
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15851

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Best Local Similarity 50.5%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 258; Indels 2; Gaps 2;

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QY 279 TATACATAATTATAAATAATTCGATCGGATAGTGTGTCGAAGTCAAGTCACATGAAT 338
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QY 399 AATATAAACAACATTTTATTTTAAATGTTGTCATTAATAATATTTTAAATTTTCAGCAC 458
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QY 459 AACAATTCACATCTCATCATTAATAATTTAATCTTATTTACCATTAATTTGAGGACA 518
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QY 519 ATTATTTTATATCTCACCTCCATTAATGCAATATTTAATTTT 563
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RESULT 5
US-09-949-016-15852/c
; Sequence 15852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15852
; LENGTH: 205044
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15852

Query Match 9.0%; Score 88.2; DB 4; Length 205044;
Best Local Similarity 50.5%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 258; Indels 2; Gaps 2;

QY 40 TCAAGTGGCACCACAAATTTTATTTTACCTCCCTGCTAGATTCGTAATACTATTGCAATTT 99
Db 201172 TCATGTTTCATAGATAGGGGTCAATTCCTCAATTAATAATATATTCAAATATTAATATATTT 201113
QY 100 ATCTCATTTTCATTTATTTTAAATTTTATTTTATTTTATTTTGGATAAAATCTAATACTTT 159
Db 201112 ATATTTAAATATATAAATATATATTTTATATATTTTATATTTTAAATATATATATTTTAT 201053
QY 160 ACTTTTTTTTAAAGAAATTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTT 219
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QY 279 TATACATAATTATAAATAATTCGATCGGATAGTGTGTCGAAGTCAAGTCACATGAAT 338
Db 200932 TTATATATTTATTTTAAATATATATATTTTATATATTTTATATTTTAAATATATATAT 200873
QY 339 TTTGTTGGAGAAAAATAAATAATTAACACATTTTTCGATTAATTTTATATATAAT 398
Db 200872 TTTTATATATTTTATTTTAAATATATAAATTAATAATATTTTATTTTATTTTAAATATATA 200814

Db 171180 ATATATATAAATATATTTTATATATATTTTAAATATATATAAATATATATTTTATATA 171121
QY 519 ATTATTTTTTAATCTCACCTCCCAATTAATGCAATATTTAAATTTT 563
Db 171120 TTTATATTTAAATATATAAATATATTTTATATATTTTATATATTTT 171076

RESULT 8
US-09-949-016-12724/c
; Sequence 12724, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12724
; LENGTH: 223471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12724

Query Match 9.0%; Score 88.2; DB 4; Length 223471;
Best Local Similarity 50.5%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 258; Indels 2; Gaps 2;
QY 40 TCAAGTGGCACCACCAATTTTTTATTTTACCTCGCTAGATTCGTAATACTATTGCAATTT 99
Db 171599 TCATGTTTCATAGATAGGGGTCAATTCCTCAATTTAAATATATTTCAAAATATTAATATATTT 171540
QY 100 ATCTCATTTTCATTTATTTTAAATTTTATATATTTTGGATATAAAATTTCTAAATCTTT 159
Db 171539 ATATTTAAATATATAAATATATTTTATATATTTTAAATATATATTTTAAATATATATTTTAT 171480
QY 160 ACTTTTTTTTAAAGAAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 219
Db 171479 ATATTTTATTTTAAATATATATATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTT 171420
QY 220 CTTTACTTTTTTTTAAAGAA-ATTTCAATTCGGTTTTTCTTAATTTAGTTTAAATTC 278
Db 171419 ATATATTTTATTTTAAATATATATATTTTATATATTTTATATTTTATTTTAAATATATATATTT 171360
QY 279 TATACATAATATAAATTTCTGATCGGATAGTGGTGTCAAGTCAAGTCACATGAAT 338
Db 171359 TTATATATTTTATTTTAAATATATATATTTTATATATTTTATATTTTATTTTAAATATATAT 171300
QY 339 TTGTGGGAGAAAATAAATAAATTTAAACACATTTTTCGATTAATTTTATTTATATATATAAT 398
Db 171299 TTTTATATTTTATTTTAAATATATAAATATATTTTATATTTTATTTTATTTTAAATATATA 171241
QY 399 AATATAACACATTTTATTTTAAATGTTGCAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 458
Db 171240 TATTTTATATTTTATTTTAAATATATAAATATATATAAATATATTTTATATTTTATTTTAAAT 171181
QY 459 AACAAATTACACTCTCATCATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 518
Db 171180 ATATATAAATATATTTTATATTTTATTTTAAATATATAAATATATTTTATATTTTATTTTAAAT 171121
QY 519 ATTATTTTTTAATCTCACCTCCCAATTAATGCAATTTTAAATTTT 563

Db 171120 TTTATATTTAAATATATAAATATATTTTATATATTTTATATATTTTATATATTTT 171076
RESULT 9
US-09-949-016-12725/c
; Sequence 12725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12725
; LENGTH: 223471
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(223471)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12725

Query Match 9.0%; Score 88.2; DB 4; Length 223471;
Best Local Similarity 50.5%; Pred. No. 1.8e-07;
Matches 265; Conservative 0; Mismatches 258; Indels 2; Gaps 2;
QY 40 TCAAGTGGCACCACCAATTTTTTATTTTACCTCGCTAGATTCGTAATACTATTGCAATTT 99
Db 171599 TCATGTTTCATAGATAGGGGTCAATTCCTCAATTTAAATATATTTCAAAATATTAATATATTT 171540
QY 100 ATCTCATTTTCATTTATTTTAAATTTTATATATTTTGGATATAAAATTTCTAAATCTTT 159
Db 171539 ATATTTAAATATATAAATATATATTTTATATATTTTAAATATATATATTTTAAATATATATTTTAT 171480
QY 160 ACTTTTTTTTAAAGAAATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 219
Db 171479 ATATTTTATTTTAAATATATATATTTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 171420
QY 220 CTTTACTTTTTTTTAAAGAA-ATTTCAATTCGGTTTTTCTTAATTTAGTTTAAATTC 278
Db 171419 ATATATTTTATTTTAAATATATATATTTTATATATTTTATATTTTATTTTAAATATATATATTT 171360
QY 279 TATACATAATATAAATTTCTGATCGGATAGTGGTGTCAAGTCAAGTCACATGAAT 338
Db 171359 TTATATATTTTATTTTAAATATATATATTTTATATATTTTATATTTTATTTTAAATATATATAT 171300
QY 339 TTGTGGGAGAAAATAAATAAATTTAAACACATTTTTCGATTAATTTTATTTATATATAAT 398
Db 171299 TTTTATATTTTATTTTAAATATATAAATATATTTTATATTTTATTTTATTTTAAATATATA 171241
QY 399 AATATAACACATTTTATTTTAAATGTTGCAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 458
Db 171240 TATTTTATATTTTATTTTAAATATATAAATATATATAAATATATTTTATATTTTATTTTAAAT 171181
QY 459 AACAAATTACACTCTCATCATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 518
Db 171180 ATATATAAATATATTTTATATTTTATTTTAAATATATAAATATATTTTATATTTTATTTTAAAT 171121
QY 519 ATTATTTTTTAATCTCACCTCCCAATTAATGCAATTTTAAATTTT 563
Db 171120 TTTATATTTTAAATATATAAATATATTTTATATATTTTATATATTTTATATATTTT 171076

Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
JS-08-487-826B-13

	Query Match	8.8%;	Score 87;	DB 2;	Length 19124;
	Best Local Similarity	50.1%;	Pred. No. 2.2e-07;		
	Matches 252;	Conservative 0;	Mismatches 240;	Indels 11;	Gaps 1;
QY	58	TTATTTTACCTCCGCTAGATTCGTAATACATATGCAATTTATGTCATTTTCATTTATTTA	117		
DB	15878	TTTTTTTATTTATTAATTTTTTTTTTTTATTTATTAATTAATTTTTTTTATTTATTTATTTT	15819		
QY	118	TTTAAATTTATTTATATTTATTTGGATAAAAATTCCTAATCTTACTTTTTTTTAAAGAA	177		
DB	15818	TTTAAATAAATTTTTTTTATTTTATGATATATTTTTTTTTTAAACATTTTTTTTAAATTTT	15759		
QY	178	TTTTATTTAAATTTATTTATATTTATTTAGATAAAATTCCTAAATCTTTTACTTTTTTTTT	237		
DB	15758	TTTTTATTTTATGATATATATTTTTTATTTTAAATATATTTTTTCTTTTTTTTTTGTTTTT	15699		
QY	238	AAGAAATTCAAATTCGCGTTTTTCTTAATTTTGTATTTAAATCTCATATCTAATTTAAATTT	297		
DB	15698	TGATATATATTTTTTTTTTTTTTAAATGTTTTTTTTTTTTCTCTTTCTTTTATTTTTTTT	1563		
QY	298	CTGATCGGAATTAGTGTGGTCTCAAGTCAAGTCACATGAATTTTGTGGAGAAAAATTA	357		
DB	15638	ATAATCATTTTTTTTTTATATAAAATTTTTTTTTTAAATTTTTTTTTTGTATATCTTTTCAT	1557		
QY	358	AAATTTAAACACAATTTTTTCGATTAATTTATTTATATATATATAATAACACATTTTTAT	417		
DB	15578	TTTTTATTTCTATCAAAATTTATATTTTATTTATATATTTTTTTTATTTTATTTTAAATTTT	1551		

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RESULT 10
US-09-949-016-17369
; Sequence 17369, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17369
; LENGTH: 61178
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17369

Query Match      8.9%; Score 87.4; DB 4; Length 61178;
Best Local Similarity 49.9%; Pred. No. 2.1e-07;
Matches 275; Conservative 0; Mismatches 271; Indels 5; Gaps 2;

Qy 98 TTATCTCAATTCATATTTATTTAAATATTTTATTTATTTATTTAGATAAAAAATTCCTAACTAT 157
Db 21250 TAAATCTTATCTTATATAAATCTTATATATATTAATGCTCTTATATAAATAATCTTATATATAT 21309

Qy 158 TTAACTTTTTTTTTAAAAAGAAATTTATTTAAATATTTTATTTATTTATTTAGATAAAAAATTCCTAA 217
Db 21310 ATAATCTTATCTTATATAATAAATCTTATTTATATAAATAAATAATCTTATATATAATAATAA 21369

Qy 218 TACTTTTACTTTTTTTTTAAAAAGAAATTCCTAAATGCGTTTTTTTCTTAATTTAGTTTTAAAT 277
Db 21370 TCTTATCTTATTAATAATAATAATCTTATATAATAATAATAATCTTATATATAATAATAATCTTATATAAT 21429

Qy 278 CTATACTAAATATAAAAAATTCGATCGGATTAGTGTGTCGCAAGTCAAGTCAACATGAA 337
Db 21430 ATAATCTTATATAATAATAATCTTATTTTATTTATATAAATCTTA-TCTTATTTATATAAT 21488

Qy 338 TTTTGTGGAGAAAAATAAAAAATTAACACATTTTTTCGATTAATTTTATTTATATATATATAA 397
Db 21489 ATAATCTTATCTTATTAATAATAATAATCTTAATCTTATTTATATAATAATAATAATCTTATCTTA 21548

Qy 398 TAATATAAACAACATTTTTTATTTAAATGCTGCAATATAATTTTTTAAATTTAAAAATTCAGCA 457
Db 21549 TTATTAATAATAATCTTATCTTATTTATATAATAATAATAATCTTAATAATAATCTTAACTTAT 21608

Qy 458 CAACAATACACTCTCATTAATTAATTAATCTTAT ---TACCATAATTAATAATTCGTA 513
Db 21609 TATATAATAAATCTTATTAATAATAATCTTAATCTTATTAATAATAATAATCTTATTAATTTATTT 21668

Qy 514 GGACAATTTTTTTTAAATCTCACCTCCAATTAATGATATTAATTTTGTTCGATPAC 573
Db 21669 ATATAATCTTATATTTATATAATAATCTTATCTTATTTATATAATGTTATTTATTTATATAA 21728

Qy 574 TTCTTATTTCACTCCTCAACATTAATCAATTAACCCAAATTTTGAATGTTATTAATTTCTTAA 633
Db 21729 TCTTAATCTTATTAATAATAATGTTATTAATTAATAATAATCTTATCTTATTTATATAATAATCTTAT 21788

Qy 634 CTTATTCACCTA 644
Db 21789 ATTATATATA 21799

RESULT 11
US-08-487-826B-13/G

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Db 252027 ATCAAAGACCTTAATCAATACTGATCCTATTTCCTGCTCATACATAAGCATTATATTT 252086

Qy 562 TTT 564

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Db 252087 TTT 252089

Search completed: March 15, 2005, 02:00:37
Job time : 214 secs

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Result No.	Query %			Description	
	Score	Match	Length	ID	Description
1	107.4	10.9	8056	18	US-10-473-126-386
2	105.8	10.7	8056	18	US-10-473-126-240
C 3	104.8	10.6	158001	17	US-10-211-179-211
	104.4	10.6	4985	14	US-10-094-240-10
5	104.4	10.6	4985	16	US-10-056-405-10
C 6	101.6	10.3	8056	18	US-10-473-126-386
C 7	100	10.2	8056	18	US-10-473-126-240
C 8	97.8	9.9	1130	18	US-10-425-115-132399
9	96.4	9.8	3673778	16	US-10-312-841-1
10	96.2	9.8	15548	15	US-10-311-455-2128
11	95.4	9.7	6109	15	US-10-311-455-299


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; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

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Query Match	10.3%	Score 101.6	DB 18	Length 8056
Best Local Similarity	49.4%	Pred. No. 8.3e-05		
Matches 291	Conservative 0	Mismatches 296	Indels 2	Gaps 1
Qy	53	ATTTTTTATTTTACCTCCTCGTAGATTGCGTAAATCTATTGCAATTTATCTCATTTTCATT	112	
Db	2420	ATTTTTTTTTTAAATTTTCAAAAAATAATAAAATTTAATAAATTTATTTATATAAAATAAAAA	2361	
Qy	113	ATTTATTTAAATTTATTTATATTTTGGATAAAAATTTCTAATACTTTTACTTTTTTAAAA	172	
Db	2360	ATTATATTTAAAAATTAATAAAAAATTTATTTAAAAACAAAAATTAATAAATTTATTTAAA	2301	
Qy	173	AAGAAATTTATTTAAATTTTATTTATTTATTTAGATAAAAAATTTCTAATACTTTTACTTTTTT	232	
Db	2300	AATAAAATAAAATTTAAAAATTTTAAAAATTTTAAATTTTAAATATAATAAAAAATAAAT	2241	
Qy	233	TTAAAAAGAAATTTCAATTTGCGTTTTTTTCTTAAATTTAGTTTTTAATCTCATACTAATATAA	292	
Db	2240	TTTTATTAATAATTAATTAA	2181	
Qy	293	AAATTTCTGATCGGAATAGTGTGGTGTCAAAGTCAAGTCAATTTTGTGGAGAAAA	352	
Db	2180	TAAAAAT--ATAATTTTTTTTTTTTTTTTTTTTTTTTTTAAATAAAAAATAAAAAATTTATTA	2123	
Qy	353	AATAAAAAATTAACACATTTTTTCGATTAATTTATATATATATAATAATAATAACACATT	412	
Db	2122	AAATTAATTAATAATAATTAATAATTAATTTATTTATTAATTTTAAATAATTTTTTAATAAT	2063	
Qy	413	TTTTATTTAAATGTTGCTCAATAATATTTTTTAAATTTAAAAATTTTCAACACAACTTACACTCT	472	
Db	2062	TTTTTAAAAATAAAAAATAATTTAAAAATAATTTTTTATTTTAAATATATTAAAAATTTTAT	2003	
Qy	473	CATCATTTAAATTTAATCTTATTTACCATAAATTAATAATTTGTGAGGCAATTTATTTTTTAATC	532	
Db	2002	TAAATTTTAAATAAAAAATTAATAATAATTTATTTTAAATAAAATTAATTTTTTTTTTTATT	1943	
Qy	533	TCACCTCCATTAAATGCAATATTAAATTTTTGTTCGATACTCTTATTTTCACTCCCTAAC	592	
Db	1942	TATATTAATAATTAATTTATTTTTTTTTTTTTTATAAAAAATTTTATTTTATATAAAAAAAT	1883	
Qy	593	ATTAATCATTTAACCCAAATTTTGAACCTGTTAATAATTTCTTAACCTTATTCA	641	
Db	1882	AAAAATAAATTAATAATAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAA	1834	

RESULT 7
US-10-473-126-240/c
; Sequence 240, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 240

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; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-240

Query Match      10.2%; Score 100; DB 18; Length 8056;
Best Local Similarity 49.2%; Pred. No. 0.00014;
Matches 290; Conservative 0; Mismatches 297; Indels 2; Gaps 1;

QY 53 ATTTTTTATTTTACCTCGCTAGATTCGTAATACTATTGCAATTTATCTCATTTCAATT 112
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2420 ATTTTTTTTTTAAATTTTCGAAAAATAAATAATTTTAATAATTTATTTATAAATAA 2361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 113 ATTTATTTTAATTTATTTATTTATTTTGGATPAAAAATTTCTAATACTTTTTTAAA 172
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2360 ATTTATTTAAAAAATTTAAATAAAAAATTTATTTAAATCTAGAAAAATTTATTTAAA 2301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 173 AAGAAATTTATTTAAATTTATTTATTTATTTAGATAAAAAATTTCTAATACTTTTAC 232
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2300 AATPAAAAATTTAAAAAATTTAAAAATTTTTTAAATTTATTTTAAATATAAAAAATAA 2241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 233 TTAATAAGAAATTTCAATTCGGTTTTTTTCTTAAATTTAGTTTTTAATCTCTACTAATTA 292
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2240 TTTATTTAAATTTAAATTTTTTTTTTTTTTTTTTTTATTTTTTTTTTCGTTTTTAAAT 2181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 293 AAATTCGATCGGAATTAGTGTGTCGCAAGTCAAGTAATTTTGTGGAGAAAA 352
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2180 TAAAAATTTTATTTTATTTTATTTTATTTTATTTTAAATAAAAAATATAAATTTATTA 2123
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 353 AATAAAAAATTAACACATTTTTTCGATTAATTTATATATATATAATATAATAACACATT 412
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2122 AAATATATTAAATAAATTTATAATTTATTTATATAATTTTAAATAATTTTAAATAAT 2063
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 413 TTTATTTAAATGTGTCAATAATATTTTTTTAAATTTAAATAATTTTCAACACAAATTA 472
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2062 TTTTAAAAATAAAAAATAATTTAAAAATAATATTTTATTTTAAATATATTTAAAAATTTAT 2003
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 473 CATCATTAATTTAATCTTTATACCATAATAAATAATTTGTGAGGCAATTTATTTTTTA 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2002 TAAATTTTAAATAAAAAATTAATAATTTATTTTAAATAATTTATTTTTTTTTTTTAT 1943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 533 TCACCTCCCAATTAATGCATATTTATTAATTTTTTGTTCGATACTCTTATTTCACTCCTAAC 592
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1942 TATATATAAATTAATTTATTTTTTTTTTTTTTATAAAAATTTTATTTTATATAAATAA 1883
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 593 ATTAATCATTTAACCCAAATTTTGAACCTGTTATAAATTTCTTAATCTATTCA 641
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1882 AAAAAATAAATTTTAAATTAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAA 1834
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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8 T. J. Shea

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RESULTS 8
US-10-425-115-132399/c
? Sequence 132399, Application US/10425115
? Publication No. US20040214272A1
? GENERAL INFORMATION:
? APPLICANT: La Rosa, Thomas J.
? APPLICANT: Kovalic, David K.
? APPLICANT: Zhou, Yihua
? APPLICANT: Cao, Yongwei
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants
? FILE REFERENCE: 38-21(53222)B
? CURRENT APPLICATION NUMBER: US/10/425,115
? CURRENT FILING DATE: 2003-04-28
? NUMBER OF SEQ ID NOS: 369326
? SEQ ID NO 132399
? LENGTH: 1130
? TYPE: DNA
? ORGANISM: Zea mays
? FEATURE:
? NAME/KEY: unsure

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[illegible]

RESULT 12
US-10-221-613-33
; Sequence 33, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221,613
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-03-15
; 2000-03-15
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 33
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:

Query Match	9.7%;	Score 95.4;	DB 15;	Length 6109;
Best Local Similarity	49.7%;	Pred. No. 0.00055;		
Matches 296; Conservative	0;	Mismatches 296;	Indels 3;	Gaps 2;


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; NAME/KEY: unsure
; LOCATION: (214, 2796...2797, 4347)
US-10-221-613-33

Query Match          9.7%; Score 95.4; DB 17; Length 6109;
Best Local Similarity 49.7%; Pred. No. 0.00055;
Matches 296; Conservative 0; Mismatches 296; Indels 3; Gaps 2;

QY 53 ATTTTATTTTACCTCCGCTAGATTCGTAATACTATTCGATTTATCTCATTTTCAT 112
Db 1628 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1687

QY 113 ATTTATTTTAAATTTATTTATTTTGGATGATGATGATGATGATGATGATGATGAT 172
Db 1688 ATATATCGAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1747

QY 173 AAGAAATTTTAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 232
Db 1748 ATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1807

QY 233 TTAATAAGAAATTTCAATTCGGTTTTCTTAAATTTAGTTTTTAAATCTAATAATTATA 292
Db 1808 TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1865

QY 293 AAATTCGATCGGATTTAGTGGTGCAAGTCAGTCACAGAAATTTTGGTGGAGAAA 352
Db 1866 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1925

QY 353 AATAAAATTAACACATTTTCGATTAATTTATTTATTTATTTATTTATTTATTTATTT 412
Db 1926 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1984

QY 413 TTTATTTAATGTTGTCATTAATTTTAAATTTAAATTTTAAATTTTAAATTTTAAATTT 472
Db 1985 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2044

QY 473 CATCATTAATTTAAATCTTTATACCAATTAATAAATTTGAGAGACAAATTTTAAATC 532
Db 2045 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2104

QY 533 TCACCTCCATTAATGCATATTTATTTATTTTGGTTCGATCTCTTATTTCACTCCTAAC 592
Db 2105 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2164

QY 593 ATTAATCATTAACCCCAATTTGAACCTGTTATATTTTCTTAACTTATTCATTTG 647
Db 2165 ATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2219

RESULT 13
US-10-311-455-952
; Sequence 952, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Expression of Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 952
; LENGTH: 6963
; TYPE: DNA
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-952

Query Match          9.6%; Score 94.6; DB 15; Length 6963;
Best Local Similarity 49.9%; Pred. No. 0.00074;
Matches 290; Conservative 0; Mismatches 289; Indels 2; Gaps 2;

QY 53 ATTTTATTTTACCTCCGCTAGATTCGTAATACTATTTGATTTATCTCATTTTCAT 112
Db 1957 AATTTTGAATTTTCGGTTTTTAGGTTTTTTGAAGATTTTCTGTTGCTAGAGTTTAAAT 2016

QY 113 ATTTATTTTAAATTTATTTATTTTGGAT-AAAAATCTCAATCTTACTTTTAA 171
Db 2017 AGTGAATATTTAAATTTTATTTTAAATGTTTAAATGTTTAAATGTTTAAATGTTT 2076

QY 172 AAAGAATTTTAAATTTATTTATTTATTTATTTAGATAAAAAATCTAATCTTACTTTT 231
Db 2077 GTTTTTTAAAGTATTTTATTTATTTATTTATTTAAAGTATTTTATTTTATTTATTTAT 2136

QY 232 TTTAAAAAGAAATTTCAATTCGGTTTTCTTAAATTTAGTTTTTAAATCTAATAATTATA 291
Db 2137 TTTATTTTATTTGATTTTAAAGTTTTTTTATCGTTTTTAAATTTGAAATTTTATGAA 2196

QY 292 AAAATCTGATCGGATTTAGTGGTGCAAGTCAGTCACATGAATTTTGGTGGAGAAA 351
Db 2197 ATTTAGTAATATAGATTTTGGTATATTTATTTATGTATATTTACGTATATTTTATTTAT 2256

QY 352 AATAAAATTTAAACACATTTTTCGATTAATTTATTTATTTATTTATTTATTTATTTAA 411
Db 2257 AGATAAAATTTAAAGTTTTGTTTTTATTTTAAAGTTAAGATTTAAGATTTATAGAAAAG 2316

QY 412 TTTTATTTAATGTTGTCATTAATTTTAAATTTAAATTTTAAATTTTAAATTTTAAATTT 471
Db 2317 TTAATAATTTAAATTTTAAAGTTTAAAGTTTAAAGTTTAAATTTTAAATTTTAAATTT 2376

QY 472 TCATCATTAATTTTAAATCTTTATACCAATTTAAATTTGAGAGACAAATTTTAAAT 531
Db 2377 GTGGAATTAATTTTATGATTAATTTGTTTATGTAATTTTGTATTTAAAGTATATATGTA 2436

QY 532 CTCACCTCCAT-TAATGCATATTTATTTATTTTGGTTCGATCTCTTATTTTCACTCCTA 590
Db 2437 ATAAAAATTTATTAATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2496

QY 591 ACATTAATCATTAACCCCAATTTTGAACCTGTTATATAATTTCTT 631
Db 2497 AATTTTAAAAATATGAATTAATTAATTTTAAATTTT 2537

RESULT 14
US-09-960-352-11234
; Sequence 11234, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11234
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8
US-09-960-352-11234

Query Match          9.6%; Score 94.4; DB 9; Length 419;
Best Local Similarity 52.6%; Pred. No. 0.00039;
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Tue Mar 15 11:35:05 2005

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Matches 206; Conservative 0; Mismatches 186; Indels 0; Gaps 0;
QY 111 TTATTATTAAATTAATTTTATATATATTTGGATATAAAATCTTAATACCTTTTCTTTTAA 170
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 87
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 171 AAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 88 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 147
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 231 TTTTAAAAAGAAATTTCAATTCGGTCTTTTCTTTAAATTTAGTTTAAATCTTACTACTAATAT 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 148 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 207
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 291 AAAAAATCTGATCGGAATAGTGGTGCAGAGTCAAGTCAATGAATTTTGGTGGAGAA 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 208 AAAAATTTATAATTTTATAAATAATAAAAAAATTTTATATATATATTTTAAAT 267
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 351 AAAATAAAAAATTAACACACATTTTTCGATTAAATTTATATATATATATATATAATAACACA 410
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 268 TAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 327
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 411 TTTTATTTAAATCTGTGCAATATATTTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAA 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 328 ATTTTAAAAAATTTTAAAAAATATTTTATAAAAAATATTTTATATAAATAATTT 387
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 471 CTCATCAATTAATTAATCTTATACCAAT 502
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 388 TATTTTCTTTTAAATATATATATTTTAAATTTT 419
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 15

```
US-10-741-601-5746
; Sequence 5746, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0601500
; CURRENT APPLICATION NUMBER: US/10741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5746
; LENGTH: 49979
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(49979)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-601-5746
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Query Match 9.5%; Score 94; DB 18; Length 49979;
Best Local Similarity 51.8%; Pred. No. 0.0015;
Matches 264; Conservative 0; Mismatches 240; Indels 6; Gaps 2;
QY 55 TTTTATTTTACCTCCCTCGTAGATTCGTAATACTATTCGATTATCTCATTTTCATTAT 114
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28754 TTTATATTTTATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 28813
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 115 TTATTTAAATTTTATATTTTGGATAAAAAATCTAATACCTTACTTTTTTTTAAAAA 174
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28814 TAAATAATATATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAA 28873
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 175 GAATTTATTTTATTTTATATTTTATTTAGATAAAAAATCTAATACCTTACTTTTTTT 234
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28874 TGTAATATATATATATATATATTTTATATAATAATAATAATAATAATAATAATAAT 28933
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 235 AAAAGAAATTTCAATTCGGTCTTTTCTTAAATTTAGTTTAAATCTTACTAATTAATAA 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28934 ATGTAATAATTTTATATTTGTTTATATATATATA-TTATATATTTTATATAATAAT 28992
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 295 ATTCTGATCGGATTAGTGTGTCAGAGTCAAGTCACATGAATTTTGTGGAGAAAAA 354
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 28993 ATTATATTTTATATTTTATATATAATAATAATAATAATAATAATAATAATAATA 29052
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 355 TAAAAATTAACACATTTTTCGATTTAATTTATATATATATATATATATATATATATAT 414
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29053 TATATATTTAATATATCT-----ATAATATATATATATATATATATATATATATATA 29107
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 415 TATTTAATGTTGCAATAATAATTTTAAATTTTAAATTTTCAAGCAACAATTAACACTCTCA 474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29108 ATTGTACATATATTTTATATATATATATATATATATATATATATATATATATATAT 29167
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 475 TCATTAAATTTAATCTTTTATTAACCAATAATTTAAATTTGTGGAGACAATTTATTTTAAATCTC 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29168 AAATATATTTTAAATATATATAATAATTTATTTTATACATTTATTTTATATACATATTA 29227
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 535 ACCCTCCATTTAATGCATATTTATTAATTTT 564
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 29228 TATATACATTTTATATATATATATATATATATATATATATATATATATATATATAT 29257
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Search completed: March 15, 2005, 03:21:37
Job time : 615 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 14, 2005, 23:07:26 ; Search time 3170 Seconds
(without alignments)
11827.541 Million cell updates/sec

Title: US-10-089-543-2_COPY_449_1433

Perfect score: 985
Sequence: 1 gatgtgaccagtgttgag.....tgagagaatccttcacatc 985

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits 'satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	131.6	13.4	1101	9	CNS000EVL
C 2	120.2	12.2	1101	9	CNS003BD
C 3	120.2	12.2	1101	9	CNS00EVL
C 4	120.2	12.2	1352	9	AG381852
C 5	116	11.8	1200	9	CNS016CO
C 6	115	11.7	1441	9	AG396166
C 7	114.8	11.7	1275	9	CL033318
C 8	114.4	11.6	886	8	BH177277
C 9	114.4	11.6	886	9	CNS07JUX
C 10	114	11.6	1101	9	CNS00EO7
C 11	113	11.5	1542	9	AG386981
C 12	112.8	11.5	839	5	BQ151187
C 13	112	11.4	990	9	CNS006OI
C 14	111.8	11.4	1896	9	CG753083
C 15	111.6	11.3	810	9	AG486400
C 16	111.4	11.3	1029	9	AG501ZGM
C 17	111	11.3	1391	9	CG754863
C 18	111	11.3	1493	9	CL078589
C 19	110.8	11.2	1242	9	CL068807
C 20	110.6	11.2	932	9	CL479576
C 21	110.4	11.2	1378	9	AG350209
C 22	109.6	11.1	1348	9	CG749499
C 23	109.2	11.1	1172	3	CR734084
C 24	109.2	11.1	1392	9	CG757503

C 25	109	11.1	939	6	BY720774
C 26	109	11.1	1005	6	BY720774
C 27	108.8	11.0	1101	9	CNS003BB
C 28	108.8	11.0	1127	9	CL128786
C 29	108.8	11.0	1227	9	AG430010
C 30	108.6	11.0	1268	8	BZ577630
C 31	108.6	11.0	1608	9	CL118721
C 32	108.4	11.0	1015	9	CL135318
C 33	108.4	11.0	1568	9	AG321250
C 34	108.2	11.0	1228	9	CL104752
C 35	108.2	11.0	1291	9	AG430338
C 36	108	11.0	1101	9	CNS0039G
C 37	108	11.0	1224	9	CL077121
C 38	107.8	10.9	988	9	CL087333
C 39	107.6	10.9	1210	9	CG749728
C 40	107.4	10.9	1243	9	AG390983
C 41	107.2	10.9	1314	9	CL077082
C 42	107	10.9	1017	9	CL101048
C 43	107	10.9	1310	9	AG382239
C 44	106.8	10.8	1201	9	CNS0167M
C 45	106.6	10.8	674	7	CV117970

ALIGNMENTS

RESULT 1
CNS000EVL/c 1101 bp DNA linear GSS 04-JUN-1999
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ACCESSION AL069706

VERSION AL069706.1 GI:4949849

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 1101)

Genoscope.

AUTHORS Direct Submission

TITLE Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooeogawa and Aaron Mammoss in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Location/Qualifiers
1..1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone_lib="BACR29B23"
/note="end : T7"

ORIGIN

Query Match 13.4%; Score 131.6; DB 9; Length 1101;
Best Local Similarity 35.6%; Pred. No. 7.5e-11;

[illegible]

172 AAAGAATTATTAATTAATTTATATTTATATTTATAGATAAATAATCTAATCTACTTCTTTT 231
|||||
847 TTTNTTTTATTTTGAATAATTTTATATTTATATTTATAGTTTATTTATTTTATTTT 906
|||||
232 TTTTAAAGAAATTCGAATTCGCTTTTCTTAATTTAGTTTAAATCTATATACTAATATA 291
|||||
907 ATTATTTATATATTTTATATATTAATTAATTTATTTTAAATTTTAAATTTAATTTAT 966
|||||
292 AAAAATCTGATCGGATAGTGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 351
|||||
967 AAAATTTTATATATTTTATATTTTATATTTTATATTTTATATTTTATATTTTATTT 1026
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352 AAATAAAATTAACACATTTTCGATTAATTTATATATATATATATATATATATATACAT 411
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1027 ATTTTAAATTTATTTTATATATTTTATATTTTATATATATATATATATATATATTT 1086
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412 TTTTATTTATGTTGTCATATATTTTATATTTTATATTTTATATTTTATATTTTATTT 471
|||||
1087 TTTTATTTTATTTTATATTTTATATTTTATATTTTATATTTTATATTTTATTTTATTT 1146
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472 TCATCAATTAATTAATCTATATACATTAATTAATTAATTTGAGGACATTTTATTTTAT 531
|||||
1147 ATTTTATTTATATATATATATATATATTTTATATTTTATATTTTATATTTTATTTT 1206
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532 CTACCTCTCAATTAATGATATATTTTATATTTTATATTTTATATTTTATATTTTATTT 591
|||||
1207 TTCTCTCTATTTTATCCCTTTATTTCTTTTATTTTATTTTATTTTATTTTATTTTATTT 1266
|||||
592 CATTAAATCAATTAACCAATTTGAATCTGTTTATATTTTATTTTATTTTATTTTATTT 639
|||||
1267 CATCACTATCTACTATTTTCTCTCTTATATTTTATTTTATTTTATTTTATTTTATTT 1314
|||||

RESULT 5
CNS016CO 1200 bp DNA linear GSS 26-JUL-1999
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15E04 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL106578
VERSION AL106578.1 GI:5622626
KEYWORDS
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1200)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelosBAC11.
FEATURES
1. 1200
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15E04"
/clone_lib="DrosBAC"
/plasmid="pBelosBAC11"
/note="end : 17"

ORIGIN
Query Match 11.8%; Score 116; DB 9; Length 1200;

Best Local Similarity 39.6%; Pred. No. 1.9e-08;
Matches 164; Conservative 86; Mismatches 164; Indels 0; Gaps 0;

QY 114 TTTATTTAAATTTATATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 173
|||||
DB 1200 TATATTTAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1141
|||||
QY 174 AGAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 233
|||||
DB 1140 AWAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAA 1081
|||||
QY 234 TAAAAAGAAATTTCAATTTGCGTTTCTTAATTTAGTTTAAATCTATATACTAATATAAA 293
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DB 1080 TTTTWTTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1021
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QY 294 AATTTCTGATCGGATAGTGGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 353
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DB 1020 TATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAA 961
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QY 354 ATAAAAATTTAAACACATTTTTCGATTAATTTATTTATTTATTTATTTATTTATTTATTT 413
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DB 960 TTAATTTWAAAAAAWATTTTWTTRTTWAAATTTAAATTTTAAATTTTTCGTTAAWATTA 901
|||||
QY 414 TTATTTAATGTTGTCATATATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 473
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DB 900 WTCHTTATTTTWTARAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 841
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QY 474 ATCATTTAAATTTAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 527
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DB 840 AACTTTWAGHAARGCYYYAMCCCKKKKKKKTTTTTTTGGGGGGGGKKKTTY 787
|||||

RESULT 6
AG396166 1441 bp DNA linear GSS 03-JUN-2004
LOCUS
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-216D06.TJ, genomic survey sequence.
ACCESSION AG396166
VERSION AG396166.1 GI:48029247
KEYWORDS GSS.
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
2 (bases 1 to 1441)
Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : TJ
LIBRARY : pBACE3.6
Vector : pBACE3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI
Location/Qualifiers
1. 1441
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"

FEATURES
source

[illegible]

COMMENT
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp

PRIMERS
Sequencing : TJ
LIBRARY

Vector : pBAC3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

FEATURES
source

Location/Qualifiers

1..1542

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMg01-201G10.TJ"

/sex="male"

/tissue_type="mixture of kidney and spleen"

/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN

Query Match 11.5%; Score 113; DB 9; Length 1542;

Best Local Similarity 49.3%; Pred. No. 5.3e-08; Indels 0; Gaps 0; Matches 290; Conservative 0; Mismatches 298;

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QY 52 AATTGTTTATTTTACCTCGCTCGCTAGATTGCTAAATCTATTGCAATTAATCTATTCATTCAT 111
Db 324 ATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 383
QY 112 TATTATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 171
Db 384 TATATATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 443
QY 172 AAGCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 231
Db 444 TTTTATAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 503
QY 232 TTTTAAAGAAATTTCAATTCGGTTTCTTAATTTAGTTTAAATTTCTATACCTAAATTA 291
Db 504 TATATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTA 563
QY 292 AAAATTCGATCGATTTAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 351
Db 564 ATATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 623
QY 352 AAATAAAATTTAAACAAATTTTTCGATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 411
Db 624 TTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 683
QY 412 TTTTATTAATGTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 471
Db 684 ATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 743
QY 472 TCATCATTAATTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 531
Db 744 TTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 803
QY 532 CTCACCTCCCAATTAATGATATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 591
Db 804 ATATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 863
QY 592 CATTAATCAATTAACCAATTTTGAACGTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 639
Db 864 ATATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 911

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RESULT 12

BQ151187

LOCUS

BQ151187

839 bp

mRNA

linear

EST 24-APR-2002

DEFINITION NF048A07LF1F1050 Developing leaf Medicago truncatula cDNA clone

ACCESSION NF048A07LF 5', mRNA sequence.

VERSION BQ151187

KEYWORDS BQ151187.1 GI:20288246

SOURCE EST.

ORGANISM Medicago truncatula (barrel medic)

Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

REFERENCE 1 (bases 1 to 839)

AUTHORS Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Imman,J.T., Wellier,J.W. and May,G.D.

TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL Medicago truncatula leaf library

COMMENT Unpublished (2000)

Contact: May GD

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 224 6650

Fax: 580 224 6692

Email: gdmay@noble.org

Insert Length: 839 Std Error: 0.00

Plate: 048 row: A column: 07

Seq primer: TCACACGAGAAACAGCTATGAC.

FEATURES

source

1..839

/organism="Medicago truncatula"

/mol_type="mRNA"

/db_xref="taxon:3880"

/clone="NF048A07LF"

/tissue_type="leaf"

/dev_stage="Pooled developmental"

/clone_lib="Developing leaf"

/note="Vector: Lambda Zap; Contains a mixture of very

young, developing, mature and senescing leaves."

ORIGIN

Query Match 11.5%; Score 112.8; DB 5; Length 839;

Best Local Similarity 50.7%; Pred. No. 6.3e-08;

Matches 298; Conservative 0; Mismatches 287; Indels 3; Gaps 1;

```

QY 54 TTTTATTTTACCTCGCTCGCTAGATTGCTAAATCTATTGCAATTAATCTATTCATTCATTA 113
Db 174 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 233
QY 114 TTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 173
Db 234 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 293
QY 174 AGAATTTATTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 233
Db 294 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 353
QY 234 TTTTATTTTAAATTTTCAATTCGGTTTCTTAATTTAGTTTAAATTTCTATACCTAAATTA 293
Db 354 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTA 413
QY 294 AATTCGATCGGATTTAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 353
Db 414 ATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 473
QY 354 ATAAATTTAAACACATTTTTCGATTAATTTTATTTATTTATTTATTTATTTATTTATTTAA 413
Db 474 ATTTAAATTTATATATCCATAATATTTTATTTATTTTATTTTATTTTATTTTATTTTAAATTA 533
QY 414 TTTTAAATTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 473
Db 534 TTTTATTTTATATAATAATAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTT 593
QY 474 ATCAATTAATTTTAACTTCTATTACCATAATAATAATAATAATAATAATAATAATAATAATA 533

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